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OM protein - protein search, using sw model			
Run on:	January 7, 2002, 15:49:10 : Search time 101.89 Seconds		
Title:	US-08-569-749-9		
Perfect score:	295		
Sequence:	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48		
Scoring table:	BIOSUM62		
	Gapop 10.0 , Gapext 0.5		
Searched:	219241 seqs, 76174552 residues		
Total number of hits satisfying chosen parameters:	219241		
Minimum DB seq length: 0			
Maximum DB seq length: 200000000			
Post-processing:	Minimum Match 0%		
	Maximum Match 100%		
	Listing first 45 summaries		
Database:	PIR 6.8:*		
	1: pirl:*		
	2: pirl2:*		
	3: pirl3:*		
	4: pirl4:*		
Pred. No.:	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	95.9	618 2 S68450	apoptosis inhibitor hasp-2 - human
2	95.6	358 2 JC5964	C;Species: Homo sapiens (man)
3	95.6	604 2 S68449	C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
4	95.6	671 2 T10304	C;Accession: S68450
5	98	671 2 A53989	R;Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraba
5	98	268 2 A53989	Nature 379, 349-353, 1996
5	98	268 2 A53989	A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of
5	98	268 2 A53989	A;Reference: number: A51822; MUID: 96149249
5	98	268 2 A53989	A;Status: nucleic acid sequence not shown
5	98	268 2 A53989	A;Molecule type: mRNA
5	98	268 2 A53989	A;Residues: 1-618 <LIS>
5	98	268 2 A53989	A;Cross-references: EMBL:045879; NID:91184317; PID:91184317; PID:AMC50372.1; PID:91184318
5	98	268 2 A53989	C;Function: apoptosis suppressor
5	98	268 2 A53989	C;Superfamily: RING finger homology
5	98	268 2 A53989	C;Keywords: apoptosis; zinc finger
5	98	268 2 A53989	F;567-611/Domain: RING finger homology <RNG>
ALIGNMENTS			
Result No.	Score	Query Match Length DB ID	Description
1	95.9	618 2 S68450	apoptosis inhibitor hasp-2 - human
2	95.6	358 2 JC5964	C;Species: Homo sapiens (man)
3	95.6	604 2 S68449	C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
4	95.6	671 2 T10304	C;Accession: S68450
5	98	671 2 A53989	R;Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Faraba
5	98	268 2 A53989	Nature 379, 349-353, 1996
5	98	268 2 A53989	A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of
5	98	268 2 A53989	A;Reference: number: A51822; MUID: 96149249
5	98	268 2 A53989	A;Status: nucleic acid sequence not shown
5	98	268 2 A53989	A;Molecule type: mRNA
5	98	268 2 A53989	A;Residues: 1-618 <LIS>
5	98	268 2 A53989	A;Cross-references: EMBL:045879; NID:91184317; PID:91184317; PID:AMC50372.1; PID:91184318
5	98	268 2 A53989	C;Function: apoptosis suppressor
5	98	268 2 A53989	C;Superfamily: RING finger homology
5	98	268 2 A53989	C;Keywords: apoptosis; zinc finger
5	98	268 2 A53989	F;567-611/Domain: RING finger homology <RNG>
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	RESULT	2	
	QC	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
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RESULT			
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	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
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Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
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	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
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	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY	1 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 48	Db 287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334
	Db	287 PEGLASAGFYVGRNDVYKCFCGCGLCRWCESDDPWEHAKWPRCE 334	
RESULT			
Query	Match	95.9%	Score 283; DB 2; Length 618;
	Best Local Similarity	97.9%	Pred. No. 9; 9e-26; Gaps 0;
	Matches	47	Conservative 0; Mismatches 1; Indels 0;
	QY		

Y	4	LASAGFYYVGRNDVKCFCGCGGIRCLCESGSDPWEHAKWPRC	52.9%; Score 156; DB 2; Length 496; Best Local Similarity 55.6%; Pred. No. 7e-11; Mismatches 25; Conservative 6; Indels 0; Gaps 0; Matches 25; Conservative 6; Mismatches 14; Indels 0; Gaps 0;
b	231	LAQAGLYVQKIGDQVRCFHNCIGLRSWQEDPWEHAKWSPKCQ	48
b	275		
RESULT	12		
	65945	65945	Apoptosis inhibitor IAP homolog - fruit fly (<i>Drosophila melanogaster</i>)
			;Species: <i>Drosophila melanogaster</i>
			;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
			;Accession: S69545
			;Duckett, C. S.; Nava, V. E.; Gedlich, R. W.; Clem, R. J.; van Dongen, J. L.; Gilfillan, M. C.;Mbo J. 15, 2685-2694, 1996
			;Title: A conserved family of cellular genes related to the baculovirus iap gene and their products
			;Status: preliminary
			;Accession: S69545
			;Status: preliminary
			;Molecule type: mRNA
			;Residues: 1-497 <DUC>
			;Cross-references: EMBL:U32373; NID:91019116; PIDN:AAAC47155.1; PID:91019117
			;Genetics: IIP
			;Gene: IIP
			;Superfamily: apoptosis inhibitor IAP homolog; RING finger homology <RRN>
			;Best Local Similarity 55.6%; Pred. No. 7e-11; Mismatches 6; Indels 0; Gaps 0; Matches 25; Conservative 6; Mismatches 14; Indels 0; Gaps 0;
RESULT	13		
	4	LASAGFYYVGRNDVKCFCGCGGIRCLCESGSDPWEHAKWPRC	52.9%; Score 156; DB 2; Length 497; Best Local Similarity 55.6%; Pred. No. 7e-11; Mismatches 6; Indels 0; Gaps 0; Matches 25; Conservative 6; Mismatches 14; Indels 0; Gaps 0;
	233	LAQAGLYVQKIGDQVRCFHNCIGLRSWQEDPWEHAKWSPKCQ	48
	277		
RESULT	13		
	4	LASAGFYYVGRNDVKCFCGCGGIRCLCESGSDPWEHAKWPRC	40.0%; Score 118; DB 2; Length 286; Best Local Similarity 43.2%; Pred. No. 1.3e-06; Mismatches 19; Conservative 7; Indels 0; Gaps 0; Matches 19; Conservative 7; Mismatches 18; Indels 0; Gaps 0;
	277		
QY	4	LASAGFYYVGRNDVKCFCGCGGIRCLCESGSDPWEHAKWPRC	47
	153	IARRGLYVQKIGDQVRCFHNCIGLRSWQEDPWEHAKWSPKCQ	47
	196		
RESULT	15		
	731067	731067	BIR repeat containing ubiquitin-conjugating enzyme BRUCE - mouse
			;C.Species: <i>Mus musculus</i> (house mouse)
			;C.Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
			;C.Accession: T30067
			;R.Hauser, H. P.; Hardroff, M.; Pyrowolakis, G.; Jentsch, S.
			;J. Cell Biol. 141, 1415-1422, 1998
			;Title: A giant ubiquitin-conjugating enzyme related to IAP apoptosis inhibitors.
			;A.Reference number: Z20963; MUID:9829517
			;A.Accession: T30067
			;A.Status: preliminary; translated from GB/EMBL/DDJB
			;A.Molecule type: mRNA
			;A.Residues: 1-4815 <HAU>
			;A.Cross-references: EMBL:Y17267; NID:93319989; PIDN:CAA76720.1; PID:93319990
			;A.Note: localized to the Golgi compartment and the vesicular system
			C.Keywords: membrane-associated protein
			Query Match
			;Best Local Similarity 42.2%; Pred. No. 5.5e-07; Mismatches 19; Indels 0; Gaps 0; Matches 21; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
Query Match	40.3%	40.3%; Score 119; DB 2; Length 150; Best Local Similarity 42.2%; Pred. No. 5.5e-07; Mismatches 19; Indels 0; Gaps 0;	
	3	OLASAGFYYVGRNDVKCFCGCGGIRCLCESGSDPWEHAKWPRC	39.8%; Score 117.5; DB 2; Length 4845; Best Local Similarity 42.0%; Pred. No. 1.9e-05; Mismatches 21; Conservative 6; Indels 3; Gaps 1; Matches 21; Conservative 6; Mismatches 20; Indels 3; Gaps 1;
	47		
QY	1	PEOLASAGFYY--VGRNDVKCFCGCGGIRCLCESGSDPWEHAKWPRC	47
	281	PLCAGFYYVGRNDVKCFCGCGGIRCLCESGSDPWEHAKWPRC	30
	36	RLCBAAGFYYVGRNDVKCFCGCGGIRCLCESGSDPWEHAKWSPNC	80
	80		
RESULT	14		
	656828	656828	R.Branasel, S. C.; Daniel, K. D.; Reilly, L. M.; Guarino, L.A.; Hong, T.; Summers, M D
			;Species: <i>Autographa californica</i> nuclear polyhedrosis virus, AcMNPV
			;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Nov-2000
			;Accession: D36828
			VPI of rotavirus.
			A.Reference number: A44221; MUID:93079853
			A.Accession: D36828
			A.Status: preliminary
			A.Molecule type: DNA
			A.Residues: 1-286
			A.Cross-references: GB:525669
			R.Ayers, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
			;Virology 202, 586-605, 1994
			;A.Title: The complete DNA sequence of <i>Autographa californica</i> nuclear polyhedrosis virus
			;A.Reference number: A72850; MUID:94303173
			A.Accession: C72853
			A.Status: preliminary
			A.Molecule type: DNA
			A.Residues: 1-199; L, 201-286 <AVR>
			A.Cross-references: GB:L22858; NID:9510708; PIDN:AAA66657.1; PID:9559096
			C.Genetics: Ac-MPL
			C.Superfamily: viral apoptosis inhibitor IAP; RING finger homology
			Query Match
			;Best Local Similarity 43.2%; Pred. No. 1.3e-06; Mismatches 19; Conservative 7; Indels 0; Gaps 0; Matches 19; Conservative 7; Mismatches 18; Indels 0; Gaps 0;
QY	4	LASAGFYYVGRNDVKCFCGCGGIRCLCESGSDPWEHAKWPRC	40.0%; Score 118; DB 2; Length 286; Best Local Similarity 43.2%; Pred. No. 1.3e-06; Mismatches 19; Conservative 7; Indels 0; Gaps 0; Matches 19; Conservative 7; Mismatches 18; Indels 0; Gaps 0;
	277		
DB	153	IARRGLYVQKIGDQVRCFHNCIGLRSWQEDPWEHAKWSPKCQ	47
	196		
RESULT	15		
	731067	731067	BIR repeat containing ubiquitin-conjugating enzyme BRUCE - mouse
			;C.Species: <i>Mus musculus</i> (house mouse)
			;C.Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
			;C.Accession: T30067
			;R.Hauser, H. P.; Hardroff, M.; Pyrowolakis, G.; Jentsch, S.
			;J. Cell Biol. 141, 1415-1422, 1998
			;Title: A giant ubiquitin-conjugating enzyme related to IAP apoptosis inhibitors.
			;A.Reference number: Z20963; MUID:9829517
			;A.Accession: T30067
			;A.Status: preliminary; translated from GB/EMBL/DDJB
			;A.Molecule type: mRNA
			;A.Residues: 1-4815 <HAU>
			;A.Cross-references: EMBL:Y17267; NID:93319989; PIDN:CAA76720.1; PID:93319990
			;A.Note: localized to the Golgi compartment and the vesicular system
			C.Keywords: membrane-associated protein
			Query Match
			;Best Local Similarity 42.2%; Pred. No. 5.5e-07; Mismatches 19; Indels 0; Gaps 0; Matches 21; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
QY	1	PEOLASAGFYY--VGRNDVKCFCGCGGIRCLCESGSDPWEHAKWPRC	39.8%; Score 117.5; DB 2; Length 4845; Best Local Similarity 42.0%; Pred. No. 1.9e-05; Mismatches 21; Conservative 6; Indels 3; Gaps 1; Matches 21; Conservative 6; Mismatches 20; Indels 3; Gaps 1;
	281	PLCAGFYYVGRNDVKCFCGCGGIRCLCESGSDPWEHAKWPRC	30
	36	RLCBAAGFYYVGRNDVKCFCGCGGIRCLCESGSDPWEHAKWSPNC	80
	80		
			Search completed: January 7, 2002, 15:49:10
			Job time: 704 sec

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